

FIG. 1

1	CTCTAGATGTACATGGAGGATGACCGAAAAAACCAATGGTGTGAAGAGCTCCCCAGCCAA	60
51	M T E K T N G V K S S P A N	14
61	TAATCACAACCATCATGCACCTCTGCCAATCAAGGCCAATGGCAAGATGACCAAGGAC	120
15	N H N H H A P P A I K A N G K D D H R T	34
121	AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCCTCAGAACTGCAGAGGCTGGC	180
35	S S R P H S A A D D D T S S E L Q R L A	54
181	AGACGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCGCGAGGATAGTTGCGCTGGTGGG	240
55	D V D A P Q Q G R S G F R R I V R L V G	74
241	GATCATCAGAGAATGGGCCAACAGAATTTCCGAGGAGGAAACCTAGGCCTGACTCATT	300
75	I I R E W A N K N F R E E E P R P D S F	94
301	CCTCGAGCGTTTTCGTGGGCTGAACTCCAGACTGTGACCACACAGGAGGGGATGGCAA	360
95	L E R F R G P E L Q T V T T Q E G D G K	114
361	AGGCGACAAGGATGGCGAGGACAAAGGCACCAAGAAGAAATTTGAACATTTGTCTTGA	420
115	G D K D G E D K G T K K K F E L F V L D	134
421	CCCGCTGGGGATTGTACTACTGCTGGCTATTTGTCTATTCGCATGCCGCTCCTTTACAA	480
135	P A G D L Y Y C W L F V I A M P V L Y N	154
481	CTGGTGCCTGCTGGTGGCCAGAGCCTGCTTCAGTGACCTACAGAAAGGCTACTACCTGGT	540
155	W C L L V A R A C F S D L Q K G Y Y L V	174
541	GTGGCTGGTGTGCTGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCGGATT	600
175	W L V L D Y V S D V V Y I A D L F I R L	194
601	GCGCACAGTTTCTCGAGCAGGGGCTGCTGGTCAAGATACCAAGAACTGCGAGACAA	660
195	R T G F L E Q G L L V K D T K K L R D N	214
661	CTACATCCACACCTGCAGTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT	720
215	Y I H T L Q F K L D V A S I I P T D L I	234
721	CTATTTGTCTGGACATCCACAGCCCTGAGGTGGCTTCAACCGCTGCTGCACCTTTCG	780
235	Y F A V D I H S P E V R F N R L L H F A	254
781	CCGCGATGTTGAGTTCTTTGACCGACAGACACGCCAACCTACCTTACATCTTCGG	840
255	R M F E F F D R T E T R T N Y P N I F R	274
841	CATCAGCAACCTTGTCCTCTACATCTTGGTCATCATCCACTGGAATGCCCTGCATCTATTA	900
275	I S N L V L Y I L V I I H W N A C I Y Y	294
901	TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGTTTACCCAAACATCATGA	960
295	A I S K S I G F G V D T W V Y P N I T D	314

FIG. 1 (Cont'd)

961	CCCTGAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCTTTACTGGTCCACACTGAC	1020
315	P E Y G Y L A R E Y I Y C L Y W S T L T	334
1021	TCCTACTACCATTGGGGAGACACCACCCCTGTAAAGGATGAGGAGTACCTATTGTGCAT	1080
335	L T T I G E T P P P V K D E E Y L F V I	354
1081	CTTTGACTTCCTGATTGGGTCCTCATCTTTGCCACCATCGTGGGAATGTGGGCTCCAT	1140
355	F D F L I G V L I F A T I V G N V G S M	374
1141	GATCTCCAACATGAATGCCACCCGGGCAGTTCAGGGCTAAGATCGATGCGTGAACA	1200
375	I S N M N A T R A E F Q A K I D A V K H	394
1201	CTACATGAGTTCGAAAGGTCAGCAAGGGGATGGAAGCCAAAGTCATTAGTGTTTGA	1260
395	Y M Q F R K V S K G M E A K V I R W F D	414
1261	CTACTTGTGGACCAATAAGAAGACAGTGATGAGCGAGAAATTCCTCAAGATCTGCCAGC	1320
415	Y L W T N K K T V D E R E I L K N L P A	434
1321	CAAGCTCAGGGCTGAGATAGCCACCAATGTCCACTTGTCACACTCAAGAAAGTCGCAT	1380
435	K L R A E I A T N V H L S T L K K V R I	454
1381	CTTCATGATTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAACTCCGTCTCAGGT	1440
455	F H D C E A G L L V E L V L K L R P Q V	474
1441	CTTCAGTCTGGGATTACATTTGCGCGAAAGGGGACATCGGCAAGGATCTACATCAT	1500
475	F S P G D Y I C R K G D I G K E M Y I I	494
1501	TAAGGAGGGCAAAGTGGCAGTGGTGGCTGATGATGCTGTGACTCAGTATGCTCTGCTGTC	1560
495	K E G K L A V V A D D G V T Q Y A L L S	514
1561	GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAAGGSCAGTAAATGGGCAA	1620
515	A G S C F G E I S I L N I K G S K M G N	534
1621	TCGACGCACAGCTAATATCCGCGAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCCAAGGA	1680
535	R R T A N I R S L G Y S D L F C L S K D	554
1681	TGATCTTATGGAAGCTGTGACTGACTACCTGATGCCAAGAAAGTCTAGAAGAGAGGGG	1740
555	D L M E A V T E Y P D A K K V L E E R G	574
1741	TCGGGAGATCTCATGAAGGAGGGACTGCTGGATGAGAACGAAGTGGCAACACGACATGGA	1800
575	R E I L M K E G L L D E N E V A T S M E	594
1801	GGTCGACGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAACCTTGTACACTCG	1860
595	V D V Q E K L G Q L E T N M E T L Y T R	614
1861	CTTTGGCGGCTGCTGGTGAGTACACGGGGGCCAGCAGAAGCTCAAGCAGCGCATCAC	1920
615	F G R L L A E Y T G A Q Q K L K Q R I T	634

FIG. 1 (Cont'd)

1921	AGTTCTGGAACCAAGATGAAACAGAACAAATGAAGATGACTACCTGTCTGATGGGATGAA	1980
635	V L E T K M K Q N N E D D Y L S D G M N	654
1981	CAGCCCTGAGCTGGCTGCTGCTGACGAGCCATAAGACCTGGGGCCCACTGCCTCTCCAG	2040
655	S F E L A A A D E P	664
2041	CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTAGATCTCCGGATTACAT	2100
2101	GCATTACCCTCATGTTCCCTGAATTCTCCAAAAGTCTCTCTGACCCTGNGTTTTTTGGCC	2160
2161	TAAACATCCAAGATTCGCGCTCGGAT	2186

1921
 1980
 635
 654
 664
 2040
 2100
 2160
 2186

FIG. 2

MTEKTNGVKSSPANNHHHAPFAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDAFPQQGRSGFRRI
 VRLVGIIREWANKNFREEEPRPDSFLERFRGPQLTVTTQEGDGKGDGEDKGTKKKKFLFVLDPAGD
 LYWCWLFVIAMPVLYNWCLLVARACFSDLQKGYLLVWLVLVDYSDVVIADLFIRLRTGFLEQGGLLVKD
 TKKLRDNYIHTLQFKLDVASIIPDLYFAVDIHSPEVRFNRLLHFARMFEFFDRTETRTNYPNIFRIS
 NLVLYILVLIHWNACIYYAISKSIGFVDTWVYPNITDPEYGYLAREYIYCLYWSTLTLTTIGETPPPV
 KDEEYLFVIFDFLIGVLI FATIVGNVGS MISNMNATRAEFQAKI DAVKHYMQFRKVS KGMEAKVIRWFD
 YLWTNKKTVDEREILKNLPALRAEIATNVHLSTLKKVRI FHDCEAGLLVELVLKLRPQVFSPGDYICR
 KGDIGKEMYIIKEGLAVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRRTANIRSLGYSDFCLS
 KDDLMEAVTEYDPAKKVLEERGREILMKEGLLDENEVATSMEDVDVQEKLGQLETNMETLYTRFGRLLAE
 YTGAQQKLKQRITVLETKMKQNNEDDYLSDGMNSPELAAADEP

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 9900
 10000

FIG. 3

MTEKTNGVKSSPANNHHHAPPAIKANGKDDHRTSSRPHSAADDDTSSELQRLADVDPQQGRSGFRRI
 VRLVGIIREWANKNFREEEPFDSFLERFRGPELQTVTTQEGDGKGDGDKGDKKKKFFELFVLDPAGD
 LY~~YCWL~~FVIAMPVLYNWCLLVARACFSDLQKGYLLVWLVLVDYVSDVVYIADLFI~~RLRT~~GFLEQGLLVKD
 TKKLRDNYIHTLQF~~KLD~~VASIIPTDLIYFAVDIHSPEVRFNRLHFARMFEFFDRTETRTNYPNIFRIS
 NLVLVILV~~II~~HWNACIYYAISKSIGFGVDTWVYPNITDPEYGYIAREYIYCLYWSTLTTLTIGETPPPV
 KDEEYLFVIFD~~FLIG~~VLI~~FATIV~~GNVGSMTISNMNATRAEFOAKIDAVKHYMQFRKVS~~KG~~MEAKVIRWFD
 YLWTKKTVDEREILKNLPAKLRAE~~IATNV~~HLS~~TLK~~KVRI~~FHD~~CEAGLLVELVLKLRPQVFS~~PGDY~~ICR
 KGDIGKEMYIIKEGLAVVADDGVTQYALLSAGSCFGEISILNIKGSKMGNRRTANIRSLGYSDLFCLS
 KDDLMEAVTEYPD~~AKV~~LEERG~~EIL~~MKEGLLDENEVATSMEDVDQEKLGQLETNMETLYTRFGRLLAE
 YTGAQQKLKQRITVLET~~KMK~~QNNEDDYLSDGMNSPELAAADEP

FIG. 4

		1	50
HMYCNG	(1)	-----	-----
CNG2_BOS	(1)	-----	-----
CNG2_MOUSE	(1)	-----	-----
CNG2_RAT	(1)	-----	-----
zACNG	(1)	MSSWRSCARAPLSGSAWRRSAAATRRSRRLCKTKRKRWSSSGKGTPMQSTQC	
		51	100
HMYCNG	(1)	-----	-----
CNG2_BOS	(1)	-----	-----
CNG2_MOUSE	(1)	-----	-----
CNG2_RAT	(1)	-----	-----
zACNG	(51)	ETRRRAQTPCSTGHTWRTTEKSNVGVSSPANNHNNHPPATKANGKDDH	
		101	150
HMYCNG	(33)	RASSRPGSAADDDTSSELQRLADDAPOQRGGFRIRVLVGLRWAN	
CNG2_BOS	(33)	RASSRPGSAADDDTSSELQRLADDAPOQRGGFRIRVLVGLRWAN	
CNG2_MOUSE	(34)	RASSRPGSAADDDTSSELQRLADDAPOQRGGFRIRVLVGLRWAN	
CNG2_RAT	(34)	RASSRPGSAADDDTSSELQRLADDAPOQRGGFRIRVLVGLRWAN	
zACNG	(101)	RASSRPGSAADDDTSSELQRLADDAPOQRGGFRIRVLVGLRWAN	
		151	200
HMYCNG	(82)	KNFRSEEPDPSFLERFRGPELOTVTTCQDGGKDGKDGKGGTGGKTKKFELE	
CNG2_BOS	(82)	KNFRSEEPDPSFLERFRGPELOTVTTCQDGGKDGKDGKGGTGGKTKKFELE	
CNG2_MOUSE	(84)	KNFRSEEPDPSFLERFRGPELOTVTTCQDGGKDGKDGKGGTGGKTKKFELE	
CNG2_RAT	(84)	KNFRSEEPDPSFLERFRGPELOTVTTCQDGGKDGKDGKGGTGGKTKKFELE	
zACNG	(150)	KNFRSEEPDPSFLERFRGPELOTVTTCQDGGKDGKDGKGGTGGKTKKFELE	
		201	250
HMYCNG	(132)	VLDPAQDWYRWLEVIAMPVLYNWCCLVARACFSDLQGYFVWLVDYV	
CNG2_BOS	(132)	VLDPAQDWYRWLEVIAMPVLYNWCCLVARACFSDLQGYFVWLVDYV	
CNG2_MOUSE	(134)	VLDPAQDWYRWLEVIAMPVLYNWCCLVARACFSDLQGYFVWLVDYV	
CNG2_RAT	(134)	VLDPAQDWYRWLEVIAMPVLYNWCCLVARACFSDLQGYFVWLVDYV	
zACNG	(200)	VLDPAQDWYRWLEVIAMPVLYNWCCLVARACFSDLQGYFVWLVDYV	
		251	300
HMYCNG	(182)	SDVVYIADLFIRLRTGFLQGLLVKDKPKLRDNYIHTLOFKLDVASIIP	
CNG2_BOS	(182)	SDVVYIADLFIRLRTGFLQGLLVKDKPKLRDNYIHTLOFKLDVASIIP	
CNG2_MOUSE	(184)	SDVVYIADLFIRLRTGFLQGLLVKDKPKLRDNYIHTLOFKLDVASIIP	
CNG2_RAT	(184)	SDVVYIADLFIRLRTGFLQGLLVKDKPKLRDNYIHTLOFKLDVASIIP	
zACNG	(250)	SDVVYIADLFIRLRTGFLQGLLVKDKPKLRDNYIHTLOFKLDVASIIP	
		301	350
HMYCNG	(232)	DLIYFVGIHSPPEVRFNRLHFARMFEFFDRTETRTSYNPIFRISNLVLY	
CNG2_BOS	(232)	DLIYFVGIHSPPEVRFNRLHFARMFEFFDRTETRTSYNPIFRISNLVLY	
CNG2_MOUSE	(234)	DLIYFVGIHSPPEVRFNRLHFARMFEFFDRTETRTSYNPIFRISNLVLY	
CNG2_RAT	(234)	DLIYFVGIHSPPEVRFNRLHFARMFEFFDRTETRTSYNPIFRISNLVLY	
zACNG	(300)	DLIYFVGIHSPPEVRFNRLHFARMFEFFDRTETRTSYNPIFRISNLVLY	
		351	400
HMYCNG	(282)	ILVITHWNACIYYAISKSIGGVDTWVYPNITDPEYGYLAREYIYCLYWS	
CNG2_BOS	(282)	ILVITHWNACIYYAISKSIGGVDTWVYPNITDPEYGYLAREYIYCLYWS	
CNG2_MOUSE	(284)	ILVITHWNACIYYAISKSIGGVDTWVYPNITDPEYGYLAREYIYCLYWS	
CNG2_RAT	(284)	ILVITHWNACIYYAISKSIGGVDTWVYPNITDPEYGYLAREYIYCLYWS	
zACNG	(350)	ILVITHWNACIYYAISKSIGGVDTWVYPNITDPEYGYLAREYIYCLYWS	

FIG. 4 (Continued)

		401	450
HBMYCNG	(332)	TLTLTTIGETPPPVKDEEYLFVDFDLIGVLIFATVGNVGSMISNMNAT	
CNG2_BOS	(332)	TLTLTTIGETPPPVKDEEYLFVDFDLIGVLIFATVGNVGSMISNMNAT	
CNG2_MOUSE	(334)	TLTLTTIGETPPPVKDEEYLFVDFDLIGVLIFATVGNVGSMISNMNAT	
CNG2_RAT	(334)	TLTLTTIGETPPPVKDEEYLFVDFDLIGVLIFATVGNVGSMISNMNAT	
rACNG	(400)	TLTLTTIGETPPPVKDEEYLFVDFDLIGVLIFATVGNVGSMISNMNAT	
		451	500
HBMYCNG	(382)	RAEFQAKIDAVKHVMQFRKVSKEAKVTKWFDYLWTNKKTVDEREVLKN	
CNG2_BOS	(382)	RAEFQAKIDAVKHVMQFRKVSKEAKVTKWFDYLWTNKKTVDEREVLKN	
CNG2_MOUSE	(384)	RAEFQAKIDAVKHVMQFRKVSKEAKVTKWFDYLWTNKKTVDEREVLKN	
CNG2_RAT	(384)	RAEFQAKIDAVKHVMQFRKVSKEAKVTKWFDYLWTNKKTVDEREVLKN	
rACNG	(450)	RAEFQAKIDAVKHVMQFRKVSKEAKVTKWFDYLWTNKKTVDEREVLKN	
		501	550
HBMYCNG	(432)	LPAKLRAEITAINVHLSTLKKVRIQDCEAGLLVELVLKLRPQVFSFGDYI	
CNG2_BOS	(432)	LPAKLRAEITAINVHLSTLKKVRIQDCEAGLLVELVLKLRPQVFSFGDYI	
CNG2_MOUSE	(434)	LPAKLRAEITAINVHLSTLKKVRIQDCEAGLLVELVLKLRPQVFSFGDYI	
CNG2_RAT	(434)	LPAKLRAEITAINVHLSTLKKVRIQDCEAGLLVELVLKLRPQVFSFGDYI	
rACNG	(500)	LPAKLRAEITAINVHLSTLKKVRIQDCEAGLLVELVLKLRPQVFSFGDYI	
		551	600
HBMYCNG	(482)	CRKGDIGKEMYIIKEGKLAVVADDGVTOYALLSAGSCFGFISTLNKGSK	
CNG2_BOS	(482)	CRKGDIGKEMYIIKEGKLAVVADDGVTOYALLSAGSCFGFISTLNKGSK	
CNG2_MOUSE	(484)	CRKGDIGKEMYIIKEGKLAVVADDGVTOYALLSAGSCFGFISTLNKGSK	
CNG2_RAT	(484)	CRKGDIGKEMYIIKEGKLAVVADDGVTOYALLSAGSCFGFISTLNKGSK	
rACNG	(550)	CRKGDIGKEMYIIKEGKLAVVADDGVTOYALLSAGSCFGFISTLNKGSK	
		601	650
HBMYCNG	(532)	MGNRRITANIRSLGYSDFCLSKDDLMEAVTEYPAKVKLEERGRETLMKE	
CNG2_BOS	(532)	MGNRRITANIRSLGYSDFCLSKDDLMEAVTEYPAKVKLEERGRETLMKE	
CNG2_MOUSE	(534)	MGNRRITANIRSLGYSDFCLSKDDLMEAVTEYPAKVKLEERGRETLMKE	
CNG2_RAT	(534)	MGNRRITANIRSLGYSDFCLSKDDLMEAVTEYPAKVKLEERGRETLMKE	
rACNG	(600)	MGNRRITANIRSLGYSDFCLSKDDLMEAVTEYPAKVKLEERGRETLMKE	
		651	700
HBMYCNG	(582)	GLIDENEVAASMEVDVQEKLEQLETNMTLYTRFARLLAEYTGAAQQLKQ	
CNG2_BOS	(582)	GLIDENEVAASMEVDVQEKLEQLETNMTLYTRFARLLAEYTGAAQQLKQ	
CNG2_MOUSE	(584)	GLIDENEVAASMEVDVQEKLEQLETNMTLYTRFARLLAEYTGAAQQLKQ	
CNG2_RAT	(584)	GLIDENEVAASMEVDVQEKLEQLETNMTLYTRFARLLAEYTGAAQQLKQ	
rACNG	(650)	GLIDENEVAASMEVDVQEKLEQLETNMTLYTRFARLLAEYTGAAQQLKQ	
		701	733
HBMYCNG	(632)	RITVLETKMKQNTEDDYLSDGMNSPEPAAAEPP	
CNG2_BOS	(632)	RITVLETKMKQNTEDDYLSDGMNSPEPAAAEPP	
CNG2_MOUSE	(634)	RITVLETKMKQNTEDDYLSDGMNSPEPAAAEPP	
CNG2_RAT	(634)	RITVLETKMKQNTEDDYLSDGMNSPEPAAAEPP	
rACNG	(700)	RITVLETKMKQNTEDDYLSDGMNSPEPAAAEPP	

FIG. 5

1	CTCTAGATGTACATGGAGGATGACCGAAAAAACAATGGTGTGAAGAGCTCCCGACGCCAA	60
1	M T E K T N G V K S S P A N	14
61	TAATCACAACTCATGCACCTCTGCCATCAAGGCCAATGGCAAGATGACCACAGGAC	120
15	N H N H H A F P A I K A N G K D D H R T	34
121	AAGCAGCAGGCCACACTCTGCAGCTGACGATGACACCTCTCAGAACTGCAGAGGCTGGC	180
35	S S R F H S A A D D D T S S E L Q R L A	54
181	AGAAGTGGATGCCCCACAGCAGGGAAGGAGTGGCTTCGCGAGGATAGTTGGCTGGTGGG	240
55	D V D A F Q Q G R S G F R R I V R L V G	74
241	GATCATCAGAAATGGGCCAACAAGAATTTCCGAGAGGAGGAACCTAGGCTGACTCATT	300
75	I I R E W A N K N F R E E E P R P D S F	94
301	CCTCGAGCGTTTTCGTGGGCTGAACTCCAGACTGTGACACACAGGAGGGGGATGGCAA	360
95	L E R F R G P E L Q T V T T Q E G D G K	114
361	AGGCACAAAGGATGGCAGGACAAAGGCACCAAGAAGAAATTTGAACTATTTGTCTTGA	420
115	G D K D G E D K G T K K K F E L F V L D	134
421	CCCAGCTGGGGATTGTACTACTGCTGGCTATTTGTCTATGCGATGCCCGTCTTTACAA	480
135	P A G D L Y Y C W L F V I A M P V L Y N	154
481	CTGGTGCCTGCTGGTGGCCAGAGCGCTGCTTCAGTGACCTACAGAAAGCTACTACCTGGT	540
155	W C L L V A R A C F S D L Q K G Y Y L V	174
541	GTGGCTGTGCTGGATTATGTCTCAGATGTGGTCTACATTGCGGACCTCTTCATCGGATT	600
175	W L V L D Y V S D V V Y I A D L F I R L	194
601	GCGCAGAGTTTCTCGAGCAGGGGCTGCTGGTCAAAGATACCAAGAACTGCGAGACAA	660
195	R T G F L E Q G L L V K D T K K L R D N	214
661	CTACATCCACCCCTGCAGTTCAAGCTGGATGTGGCTTCCATCATCCCCACTGACCTGAT	720
215	Y I H T L Q F K L D V A S I I P T D L I	234
721	CTATTTTGTGTGGACATCCACAGCCCTGAGGTGCGCTTCAACCGCGTGTGCTCACTTTGC	780
235	Y F A V D I H S P E V R F N R L L H F A	254
781	CCGATGTTTGAGTTCTTTGACCGGACAGAGACACGCACCACTACCTAACATCTTCGG	840
255	R M F E F F D R T E T R T N Y P N I F R	274
841	CATCAGCAACCTTGTCTCTACATCTTGGTCATCATCCACTGGAATGCTGCATCTATTA	900
275	I S N L V L Y I L V I I H W N A C I Y Y	294
901	TGCCATCTCCAAATCCATAGGCTTTGGGGTCGACACCTGGGGTTACCCAAACATCACTGA	960
295	A I S K S I G F G V D T W V Y P N I T D	314

FIG. 5 (Cont'd)

961	CCTCAGTATGGCTACCTGGCTAGGGAATACATCTATTGCCCTTACTGGTCCACACTGAC	1020
315	P E Y G Y L A R E Y I Y C L Y W S T L T	334
1021	TCTCACTACCATGGGGAGACACCCACCCCTGTAAAGGATGAGGAGTACCTATTGTTCAT	1080
335	L T T I G E T P P P V K D E E Y L F V I	354
1081	CTTTGACTTCCTGATTGGCGTCTCATCTTTGCCACCATCGTGGGAAATGTGGGCTCCAT	1140
355	F D F L I G V L I F A T I V G N V G S M	374
1141	GATCTCCAACATGAATGCCACCCGGGCAGTTCAGGCTAAGATCGATCCGTGAAACA	1200
375	I S N M N A T R A E F Q A K I D A V K H	394
1201	CTACATGCAGTTCGAAAGGTCAGCAAGGGGATGGAAGCAAGGTCATTAGSTGGTTTGA	1260
395	Y M Q F R K V S K G M E A K V I R V F D	414
1261	CTACTTGTGGACCAATAAGAAGACATGGATGAGCGAGAAATCTCAAGAACTGCCAGC	1320
415	Y L W T N K K T V D E R E I L K N L P A	434
1321	CAAGCTCAGGGCTGAGATAGCCATCAATGTCCACTTGTCCACACTCAAGAAAGTCGCGCAT	1380
435	K L R A A E I A I N V H L S T L K K V R I	454
1381	CTTCCATGATTTGTGAGGCTGGCCTGCTGGTAGAGCTGGTACTGAACTCCGTCTCAGGT	1440
455	F H D C E A G L L V E L V L K L R P Q V	474
1441	CTTCAGTCTGGGGATTACATTTGCCGCAAGGGGACATCGGCAAGGAGATGTACATCAT	1500
475	F S P G D Y I C R K G D I G K E M Y I I	494
1501	TAAGGAGGCAAACTGGCAGTGGTGGCTGATGATGGTGTGACTCAGTATGCTTGTCTGTC	1560
495	K E G K L A V V A D D G V T Q Y A L L S	514
1561	GGCTGGAAGCTGCTTTGGCGAGATCAGTATCCTTAACATTAAGGGCAGTAAAAATGGCAA	1620
515	A G S C F G E I S I L N I K G S K M G N	534
1621	TGACGACACGCTAATATCCGAGCCTGGGCTACTCAGATCTCTTCTGCTGTGCCAAGGA	1680
535	R R T A N I R S L G Y S D L F C L S K D	554
1681	TGATCTTATGGAAGCTGTGACTGAGTACCCTGATGCCAAGAAAGTCTAGAAGAGAGGGG	1740
555	D L M E A V T E Y P D A K K V L E E R G	574
1741	TCGGGAGATCCTCATGAAGGAGGGACTGCTGGATGAGAAGCAAGTGGCAACCGCATGGA	1800
575	R E I L M K E G L L D E N E V A T S M E	594
1801	GGTCGAGTGCAGGAGAAGCTAGGGCAGCTGGAGACCAACATGGAACCTTGTACACTCG	1860
595	V D V Q E K L G Q L E T N M E T L Y T R	614
1861	CTTTGGCCGCTGCTGGCTGAGTACACGGGGGCCAGCAGAAGCTCAAGCAGCGCATCAC	1920
615	F G R L L A E Y T G A Q Q K L K Q R I T	634

FIG. 5 (Cont'd)

1921	AGTTCGGAAACCAAGATGAAACAGAACAAATGAAGATGACTACCTGTCTGATGGGATGAA	1980
635	V L E T K M K Q N N E D D Y L S D G M N	654
1981	CAGCCCTGAGCTGGCTGCTGCTGAOGAGCCATAAGACCTGGGGCCCACTGCCTCTCCAG	2040
655	S P E L A A A D E P	664
2041	CATTGGCCTTGGCCTTGATCCCAGAAGCTAGAGGAGCTATTTAGATCTCCGGATTACAT	2100
2101	GCATTACCCTCATGTTCCCTGAATTCTCCCAAAGCCTCTCTGACCCTGGGT'TTTTGGCC	2160
2161	TAAACATCCAAGATTCCGCCTCGGATCCCG	2190

1921
 1981
 2041
 2101
 2161

FIG. 7

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1 MTEKTINGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50
1 MTEKTINGVKSSPANNHNHHAPPAIKANGKDDHRTSSRPHSAADDDTSSEL 50

51 QRLADVADPAQQGRSGFRRIIVRLVGIIREWANKNFREEEP RPDSFLERFRG 100
51 QRLADVADPAQQGRSGFRRIIVRLVGIIREWANKNFREEEP RPDSFLERFRG 100

101 PELQIVTVTQEGDGKGDGDGEDGKTKKKFELFVLDPAGLDLYYCWL FVIAMP 150
101 PELQIVTVTQEGDGKGDGDGEDGKTKKKFELFVLDPAGLDLYYCWL FVIAMP 150

151 VLYNWCLLVARACFSDLQKGYYLVWLVDLVSDVVYIADFLIRLRTGFLE 200
151 VLYNWCLLVARACFSDLQKGYYLVWLVDLVSDVVYIADFLIRLRTGFLE 200

201 QGLLVKDTKKLRDNYIHTLQFKLDVASI IPTDLIFYAVD IHSPEVRFNRL 250
201 QGLLVKDTKKLRDNYIHTLQFKLDVASI IPTDLIFYAVD IHSPEVRFNRL 250

251 LHFARMFEPFDRTETRTNYNPIFRISNLVLYILVI IHNWACIYYAISKSI 300
251 LHFARMFEPFDRTETRTNYNPIFRISNLVLYILVI IHNWACIYYAISKSI 300

301 GFGVDTWVYFNITDPEYGYLAREYIYCLYSTLT LTTIGETPPPVKDEEY 350
301 GFGVDTWVYFNITDPEYGYLAREYIYCLYSTLT LTTIGETPPPVKDEEY 350

351 L FVIFDFLIGVLIFATIVGNVGSMSINMNATRAEFOAKIDAVKHYMQFRK 400
351 L FVIFDFLIGVLIFATIVGNVGSMSINMNATRAEFOAKIDAVKHYMQFRK 400

401 VSKGMEAKVIRWFDYLVWTKNKTVDEREILKNLP AKLRAEIAINVHLS TLK 450
401 VSKGMEAKVIRWFDYLVWTKNKTVDEREILKNLP AKLRAEIAINVHLS TLK 450

451 KVRIFHDCEAGLLVELVLKLRPQVFS PGDYICRKGDIGKEMYI IKEGKLA 500
451 KVRIFHDCEAGLLVELVLKLRPQVFS PGDYICRKGDIGKEMYI IKEGKLA 500

501 VVADDGVGTQYALLSAGSCFGEISI LNKSGSKMGNRRTANIRSLGYS DFLC 550
501 VVADDGVGTQYALLSAGSCFGEISI LNKSGSKMGNRRTANIRSLGYS DFLC 550

551 LSKDDLMEAVTEY PDAKKVLEERGEREILMKEGLLDENEVATSM EVDVQEK 600
551 LSKDDLMEAVTEY PDAKKVLEERGEREILMKEGLLDENEVATSM EVDVQEK 600

601 LGQLETNMETLYTRFGRLLAEYTG AQQKLQRITVLETMKMKONNEDDYLS 650
601 LGQLETNMETLYTRFGRLLAEYTG AQQKLQRITVLETMKMKONNEDDYLS 650

651 DGMNSPELAAADEP* 665
651 DGMNSPELAAADEP. 664

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